US005552281A

United States Patent [19]

Stashenko et al.

[11] **Patent Number: 5,552,281**

[45] **Date of Patent: Sep. 3, 1996**

[54] **HUMAN OSTEOCLAST-SPECIFIC AND -RELATED GENES**

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[21] Appl. No.: **392,678**

[22] Filed: **Feb. 23, 1995**

Related U.S. Application Data

[63] Continuation of Ser. No. 45,270, Apr. 6, 1993, abandoned.

[51] **Int. Cl.**[6] **C07H 21/04**; C12N 5/10; C12N 15/70; C12Q 1/68

[52] **U.S. Cl.** **435/6**; 435/69.1; 435/172.3; 435/252.3; 435/320.1; 536/23.1

[58] **Field of Search** 435/6, 320.1, 252.3, 435/69.1, 172.3; 536/23.1

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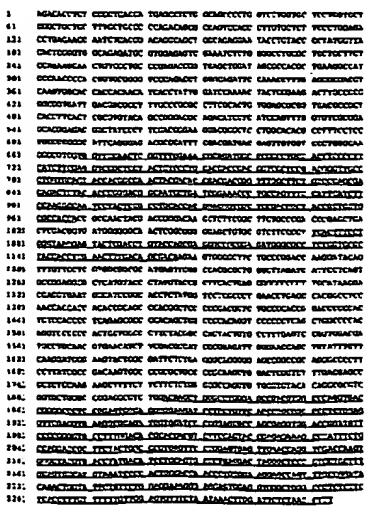
[57] **ABSTRACT**

The present invention relates to purified DNA sequences encoding all or a portion of an osteoclast-specific or -related gene products and a method for identifying such sequences. The invention also relates to antibodies directed against an osteoclast-specific or -related gene product. Also claimed are DNA constructs capable of replicating DNA encoding all or a portion of an osteoclast-specific or -related gene product, and DNA constructs capable of directing expression in a host cell of an osteoclast-specific or -related gene product.

5 Claims, 1 Drawing Sheet



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1     AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCCTG GTCCTGGTGC TCCTGGTGCT
61    GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA
121   CCTGAGAACC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA
181   CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT
241   CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT
301   GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGGCAGATTC CAAACCTTTG AGGGCGACCT
361   CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG
421   GGCGGTGATT GACGACGCCT TTGCCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCCGCT
481   CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTCGCGGA
541   GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC
601   TGGCCCCGGC ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA
661   GGGCGTCGTG GTTCCAACTC GGTTTGGAAA CGCAGATGGC GCGGCCTGCC ACTTCCCCTT
721   CATCTTCGAG GGCCGCTCCT ACTCTGCCTG CACCACCGAC GGTCGCTCCG ACGGGTTGCC
781   CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA
841   GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCATCTT
901   CCAAGGCCAA TCCTACTCCG CCTGCACCAC GGACGGTCGC TCCGACGGCT ACCGCTGGTG
961   CGCCACCACC GCCAACTACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCCGAGCTGA
1021  CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCCT TCACTTTCCT
1081  GGGTAAGGAG TACTCGACCT GTACCAGCGA GGGCCGCGGA GATGGGCGCC TCTGGTGCGC
1141  TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG
1201  TTTGTTCCTC GTGGCGGCGC ATGAGTTCGG CCACGCGCTG GGCTTAGATC ATTCCTCAGT
1261  GCCGGAGGCG CTCATGTACC CTATGTACCG CTTCACTGAG GGGCCCCCCT TGCATAAGGA
1321  CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCCTCC
1381  AACCACCACC ACACCGCAGC CCACGGCTCC CCCGACGGTC TGCCCCACCG GACCCCCCAC
1441  TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC
1501  AGGTCCCCCC ACTGCTGGCC CTTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA
1561  TGCCTGCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGGAACCAGC TGTATTTGTT
1621  CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCCGGCCGC AGGGCCCCTT
1681  CCTTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC
1741  GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC
1801  GGTGCTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC
1861  CGGGGCCCTC CGGAGTGGCA GGGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG
1921  GTTCGACGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT
1981  CCCCGGGGTG CCTTTGGACA CGCACGACGT CTTCCAGTAC CGAGAGAAAG CCTATTTCTG
2041  CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACCAGG TGGACCAAGT
2101  GGGCTACGTG ACCTATGACA TCCTGCAGTG CCCTGAGGAC TAGGGCTCCC GTCCTGCTTT
2161  GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA
2221  CAAACTGGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC
2281  TCACCTTTGT TTTTTGTTGG AGTGTTTCTA ATAAACTTGG ATTCTCTAAC CTTT
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Figure 1

HUMAN OSTEOCLAST-SPECIFIC AND -RELATED GENES

RELATED APPLICATION

This application is a continuation of application Ser. No. 08/045,270 filed on Apr. 6, 1993 now abandoned.

BACKGROUND OF THE INVENTION

Excessive bone resorption by osteoclasts contributes to the pathology of many human diseases including arthritis, osteoporosis, periodontitis, and hypercalcemia of malignancy. During resorption, osteoclasts remove both the mineral and organic components of bone (Blair, H. C., et al., *J. Cell Biol.* 102:1164 (1986)). The mineral phase is solubilized by acidification of the sub-osteoclastic lacuna, thus allowing dissolution of hydroxyapatite (Vaes, G., *Clin. Orthop. Relat.* 231:239 (1988)). However, the mechanism(s) by which type I collagen, the major structural protein of bone, is degraded remains controversial. In addition, the regulation of osteoclastic activity is only partly understood. The lack of information concerning osteoclast function is due in part to the fact that these cells are extremely difficult to isolate as pure populations in large numbers. Furthermore, there are no osteoclastic cell lines available. An approach to studying osteoclast function that permits the identification of heretofore unknown osteoclast-specific or -related genes and gene products would allow identification of genes and gene products that are involved in the resorption of bone and in the regulation of osteoclastic activity. Therefore, identification of osteclast-specific or -related genes or gene products would prove useful in developing therapeutic strategies for the treatment of disorders involving aberrant bone resorption.

SUMMARY OF THE INVENTION

The present invention relates to isolated DNA sequences encoding all or a portion of osteoclast-specific or -related gene products. The present invention further relates to DNA constructs capable of replicating DNA encoding osteoclast-specific or -related gene products. In another embodiment, the invention relates to a DNA construct capable of directing expression of all or a portion of the osteoclast-specific or -related gene product in a host cell.

Also encompassed by the present invention are prokaryotic or eukaryotic cells transformed or transfected with a DNA construct encoding all or a portion of an osteoclast-specific or -related gene product. According to a particular embodiment, these cells are capable of replicating the DNA construct comprising the DNA encoding the osteoclast-specific or -related gene product, and, optionally, are capable of expressing the osteoclast-specific or -related gene product. Also claimed are antibodies raised against osteoclast-specific or -related gene products, or portions of these gene products.

The present invention further embraces a method of identifying osteoclast-specific or -related DNA sequences and DNA sequences identified in this manner. In one embodiment, cDNA encoding osteoclast is identified as follows: First, human giant cell tumor of the bone was used to 1) construct a cDNA library; 2) produce ^{32}P-labelled cDNA to use as a stromal cell$^+$; osteoclast$^+$ probe, and 3) produce (by culturing) a stromal cell population lacking osteoclasts. The presence of osteoclasts in the giant cell tumor was confirmed by histological staining for the osteoclast marker, type 5 tartrate-resistant acid phosphatase (TRAP) and with the use of monoclonal antibody reagents.

The stromal cell population lacking osteoclasts was produced by dissociating cells of a giant cell tumor, then growing and passaging the cells in tissue culture until the cell population was homogeneous and appeared fibroblastic. The cultured stromal cell population did not contain osteoclasts. The cultured stromal cells were then used to produce a stromal cell$^+$, osteoclast$^-$ ^{32}P-labelled cDNA probe.

The cDNA library produced from the giant cell tumor of the bone was then screened in duplicate for hybridization to the cDNA probes: one screen was performed with the giant cell tumor cDNA probe (stromal cell$^+$, osteoclast$^+$), while a duplicate screen was performed using the cultured stromal cell cDNA probe (stromal cell$^+$, osteoclast$^-$). Hybridization to a stromal$^+$, osteoclast$^+$ probe, accompanied by failure to hybridize to a stromal$^+$, osteoclast$^-$ probe indicated that a clone contained nucleic acid sequences specifically expressed by osteoclasts.

In another embodiment, genomic DNA encoding osteoclast-specific or -related gene products is identified through known hybridization techniques or amplification techniques. In one embodiment, the present invention relates to a method of identifying DNA encoding an osteoclast-specific or -related protein, or gene product, by screening a cDNA library or a genomic DNA library with a DNA probe comprising one or more sequences selected from the group consisting of the DNA sequences set out in Table I (SEQ ID NOs: 1–32). Finally, the present invention relates to an osteoclast-specific or related protein encoded by a nucleotide sequence comprising a DNA sequence selected from the group consisting of the sequences set out in Table I, or their complementary strands.

BRIEF DESCRIPTION OF FIG. 1

The FIG. 1 shows cDNA sequence (SEQ ID NO: 33) of human gelatinase B, and highlights those portions of the sequence represented by the osteoclast-specific or -related cDNA clones of the present invention.

DETAILED DESCRIPTION OF THE INVENTION

As described herein, Applicant has identified osteoclast-specific or osteoclast-related nucleic acid sequences. These sequences were identified as follows: Human giant cell tumor of the bone was used to 1) construct a cDNA library; 2) produce ^{32}P-labelled cDNA to use as a stromal cell$^+$, osteoclast$^+$probe, and 3) produce (by culturing) a stromal cell population lacking osteoclasts. The presence of osteoclasts in the giant cell tumor was confirmed by histological staining for the osteoclast marker, type 5 acid phosphatase (TRAP). In addition, monoclonal antibody reagents were used to characterize the multinucleated cells in the giant cell tumor, which cells were found to have a phenotype distinct from macrophages and consistent with osteoclasts.

The stromal cell population lacking osteoclasts was produced by dissociating cells of a giant cell tumor, then growing the cells in tissue culture for at least five passages. After five passages the cultured cell population was homogeneous and appeared fibroblastic. The cultured population contained no multinucleated cells at this point, tested negative for type 5 acid phosphatase, and tested variably alkaline phosphatase positive. That is, the cultured stromal cell population did not contain osteoclasts. The cultured stromal

cells were then used to produce a stromal cell$^+$, osteoclast$^-$ ^{32}P-labelled cDNA probe.

The cDNA library produced from the giant cell tumor of the bone was then screened in duplicate for hybridization to the cDNA probes: one screen was performed with the giant cell tumor cDNA probe (stromal cell$^+$, osteroclast$^+$), while a duplicate screen was performed using the cultured stromal cell cDNA probe (stromal cell$^+$ osteoclast$^-$) Clones that hybridized to the giant cell tumor cDNA probe (stromal$^+$, osteoclast$^+$), but not to the stromal cell cDNA probe (stromal$^+$, osteoclast$^-$), were assumed to contain nucleic acid sequences specifically expressed by osteoclasts.

As a result of the differential screen described herein, DNA specifically expressed in osteoclast cells characterized as described herein was identified. This DNA, and equivalent DNA sequences, is referred to herein as osteoclast-specific or osteoclast-related DNA. Osteoclast-specific or -related DNA of the present invention can be obtained from sources in which it occurs in nature, can be produced recombinantly or synthesized chemically; it can be cDNA, genomic DNA, recombinantly-produced DNA or chemically-produced DNA. An equivalent DNA sequence is one which hybridizes, under standard hybridization conditions, to an osteoclast-specific or -related DNA identified as described herein or to a complement thereof.

Differential screening of a human osteoclastoma cDNA library was performed to identify genes specifically expressed in osteoclasts. Of 12,000 clones screened, 195 clones were identified which are either uniquely expressed in osteoclasts, or are osteoclast-related. These clones were further identified as osteoclast-specific, as evidenced by failure to hybridize to mRNA derived from a variety of unrelated human cell types, including epithelium, fibroblasts, lymphocytes, myelomonocytic cells, osteoblasts, and neuroblastoma cells. Of these, 32 clones contain novel cDNA sequences which were not found in the GenBank database.

A large number of cDNA clones obtained by this procedure were found to represent 92 kDa type IV collagenase (gelatinase B; E.C. 3.4.24.35) as well as tartrate resistant acid phosphatase. In situ hybridization localized mRNA for gelatinase B to multinucleated giant cells in human osteoclastomas. Gelatinase B immunoreactivity was demonstrated in giant cells from 8/8 osteoclastomas, osteoclasts in normal bone, and in osteoclasts of Paget's disease by use of a polyclonal antisera raised against a synthetic gelatinase B peptide. In contrast, no immunoreactivity for 72 kDa type IV collagenase (gelatinase A; E.C. 3.4.24.24), which is the product of a separate gene, was detected in osteoclastomas or normal osteoclasts.

The present invention has utility for the production and identification of nucleic acid probes useful for identifying osteoclast-specific or -related DNA. Osteoclast-specific or -related DNA of the present invention can be used to produce osteoclast-specific or -related gene products useful in the therapeutic treatment of disorders involving aberrant bone resorption. The osteoclast-specific or -related sequences are also useful for generating peptides which can then be used to produce antibodies useful for identifying osteoclast-specific or -related gene products, or for altering the activity of osteoclast-specific or -related gene products. Such antibodies are referred to as osteoclast-specific antibodies. Osteoclast-specific antibodies are also useful for identifying osteoclasts. Finally, osteoclast -specific or -related DNA sequences of the present invention are useful in gene therapy. For example, they can be used to alter the expression in osteoclasts of an aberrant osteoclast -specific or -related gene product or to correct aberrant expression of an osteoclast-specific or -related gene product. The sequences described herein can further be used to cause osteoclast-specific or related gene expression in cells in which such expression does not ordinarily occur, i.e., in cells which are not osteoclasts.

Example 1—Osteoclast cDNA Libary Construction

Messenger RNA (mRNA) obtained from a human osteoclastoma ('giant cell tumor of bone'), was used to construct an osteoclastoma cDNA library. Osteoclastomas are actively bone resorptive tumors, but are usually non-metastatic. In cryostat sections, osteoclastomas consist of ~30% multinucleated cells positive for tartrate resistant acid phosphatase (TRAP), a widely utilized phenotypic marker specific in vivo for osteoclasts (Minkin, *Calcif. Tissue Int.* 34:285–290 (1982)). The remaining cells are uncharacterized 'stromal' cells, a mixture of cell types with fibroblastic/mesenchymal morphology. Although it has not yet been definitively shown, it is generally held that the osteoclasts in these tumors are non-transformed, and are activated to resorb bone in vivo by substance(s) produced by the stromal cell element.

Monoclonal antibody reagents were used to partially characterize the surface phenotype of the multinucleated cells in the giant cell tumors of long bone. In frozen sections, all multinucleated cells expressed CD68, which has previously been reported to define an antigen specific for both osteoclasts and macrophages (Horton, M. A. and M. H. Helfrich, In Biology and Physiology of the Osteoclast, B. R. Rifkin and C. V. Gay, editors, CRC Press, Inc. Boca Raton, Fla., 33–54 (1992)). In contrast, no staining of giant cells was observed for CD11b or CD14 surface antigens, which are present on monocyte/macrophages and granulocytes (Arnaout, M. A. et al. *J. Cell. Physiol.* 137:305 (1988); Haziot, A. et al. *J. Immunol.* 141:547 (1988)). Cytocentrifuge preparations of human peripheral blood monocytes were positive for CD68, CD11b, and CD14. These results demonstrate that the multinucleated giant cells of osteoclastomas have a phenotype which is distinct from that of macrophages, and which is consistent with that of osteoclasts.

Osteoclastoma tissue was snap frozen in liquid nitrogen and used to prepare poly A$^+$ mRA according to standard methods. cDNA cloning into a pcDNAII vector was carried out using a commercially-available kit (Librarian, InVitrogen). Approximately 2.6×10^6 clones were obtained, >95% of which contained inserts of an average length 0.6 kB.

Example 2—Stromal Cell mRNA Preparation

A portion of each osteoclastoma was snap frozen in liquid nitrogen for mRNA preparation. The remainder of the tumor was dissociated using brief trypsinization and mechanical disaggregation, and placed into tissue culture. These cells were expanded in Dulbecco's MEM (high glucose, Sigma) supplemented with 10% newborn calf serum (MA Bioproducts), gentamycin (0.5 mg/ml), 1-glutamine (2 mM) and non-essential amino acids (0.1 mM) (Gibco). The stromal cell population was passaged at least five times, after which it showed a homogenous, fibroblastic looking cell population that contained no multinucleated cells. The stromal cells were mononuclear, tested negative acid phosphatase, and tested variably alkaline phosphatase positive. These findings indicate that propagated stromal cells (i.e., stromal cells that

are passaged in culture) are non-osteoclastic and non-activated.

Example 3—Identification of DNA Encoding Osteoclastoma-Specific or -Related Gene Products by Differential screening of an Ostcoclastoma cDNA Library

A total of 12,000 clones drawn from the osteoclastoma cDNA library were screened by differential hybridization, using mixed ^{32}P labelled cDNA probes derived from (1) giant cell tumor mRNA (stromal cell$^+$, OC$^+$), and (2) mRNA from stromal cells (stromal cell$^+$, OC$^+$) cultivated from the same tumor. The probes were labelled with ^{32}[P]dCTP by random priming to an activity of $\sim 10^9$CPM/μg. Of these 12,000 clones, 195 gave a positive hybridization signal with giant cell (i.e., osteoclast and stromal cell) mRNA, but not with stromal cell mRNA. Additionally, these clones failed to hybridize to cDNA produced from mRNA derived from a variety of unrelated human cell types including epithelial cells, fibroblasts, lymphocytes, myelomonocytic cells, osteoblasts, and neuroblastoma cells. The failure of these clones to hybridize to cDNA produced from mRNA derived from other cell types supports the conclusion that these clones are either uniquely expressed in osteoclasts, or are osteoclast-related.

The osteoclast (OC) cDNA library was screened for differential hybridization to OC cDNA (stromal cell$^+$, OC$^+$) and stromal cell cDNA (stromal cell$^+$, OC$^-$) as follows:

NYTRAN filters (Schleicher & Schuell) were placed on agar plates containing growth medium and ampicillin. Individual bacterial colonies from the OC library were randomly picked and transferred, in triplicate, onto filters with prerulcd grids and then onto a master agar plate. Up to 200 colonies were inoculated onto a single 90-mm filter/plate using these techniques. The plates were inverted and incubated at 37° C. until the bacterial inoculates had grown (on the filter) to a diameter of 0.5–1.0 mm.

The colonies were then lysed, and the DNA bound to the filters by first placing the filters on top of two pieces of Whatman 3 MM paper saturated with 0.5N NaOH for 5 minutes. The filters were neutralized by placing on two pieces of Whatman 3 MM paper saturated with 1M Tris-HCL, pH 8.0 for 3–5 minutes. Neutralization was followed by incubation on another set of Whatman 3 MM papers saturated with 1M Tris-HCL, pH 8.0/1.5M NaCl for 3–5 minutes. The filters were then washed briefly in 2×SSC.

DNA was immobilized on the filters by baking the filters at 80° C. for 30 minutes. Filters were best used immediately, but they could be stored for up to one week in a vacuum jar at room temperature.

Filters were prehybridized in 5–8 ml of hybridization solution per filter, for 2–4 hours in a heat sealable bag. An additional 2 ml of solution was added for each additional filter added to the hybridization bag. The hybridization buffer consisted of 5×SSC, 5×Denhardt's solution, 1% SDS and 100 μg/ml denatured heterologous DNA.

Prior to hybridization, labeled probe was denatured by heating in 1×SSC for 5 minutes at 100° C., then immediately chilled on ice. Denatured probe was added to the filters in hybridization solution, and the filters hybridized with continuous agitation for 12–20 hours at 65° C.

After hybridization, the filters were washed in 2×SSC/0.2% SDS at 50°–60° C. for 30 minutes, followed by washing in 0.2×SSC/0.2% SDS at 60° C. for 60 minutes.

The filters were then air dried and autoradiographed using an intensifying screen at −70° C. overnight.

Example 4—DNA Sequencing of Selected Clones

Clones reactive with the mixed tumor probe, but unreactive with the stromal cell probe, are expected to contain either osteoclast-related, or in vivo 'activated' stromal-cell-related gene products. One hundred and forty-four cDNA clones that hybridized to tumor cell cDNA, but not to stromal cell cDNA, were sequenced by the dideoxy chain termination method of Sanger et al. (Sanger F., et al. *Proc. Natl. Acad. Sci. USA* 74:5463 (1977)) using sequenase (US Biochemical). The DNASIS (Hitatchi) program was used to carry out sequence analysis and a homology search in the GenBank/EMBL database.

Fourteen of the 195 tumor$^+$ stromal$^-$ clones were identified as containing inserts with a sequence identical to the osteoclast marker, type 5 tartrate-resistant acid phosphatase (TRAP) (GenBank accession number J04430 M19534). The high representation of TRAP positive clones also indicates the effectiveness of the screening procedure in enriching for clones which contain osteoclast-specific or related cDNA sequences.

Interestingly, an even larger proportion of the tumor$^+$ stromal$^-$ clones (77/195; 39.5%) were identified as human gelatinase B (macrophage-derived gelatinase) (Wilhelm, S. M. *J. Biol. Chem.* 264:17213 (1989)), again indicating high expression of this enzyme by osteoclasts. Twenty-five of the gelatinase B clones were identified by dideoxy sequence analysis; all 25 showed 100% sequence homology to the published gelatinase B sequence (Genbank accession number J05070). The portions of the gelatinase B cDNA sequence covered by these clones is shown in the FIGURE (SEQ ID NO: 33). An additional 52 gelatinase B clones were identified by reactivity with a ^{32}P-labelled probe for gelatinase B.

Thirteen of the sequenced clones yielded no readable sequence. A DNASIS search of GenBank/EMBL databases revealed that, of the remaining 91 clones, 32 clones contain novel sequences which have not yet been reported in the databases or in the literature. These partial sequences are presented in Table I. Note that three of these sequences were repeats, indicating fairly frequent representation of mRNA related to this sequence. The repeat sequences are indicated by$^{a, b}$ superscripts (Clones 198B, 223B and 32C of Table I).

TABLE I

PARTIAL SEQUENCES OF 32 NOVEL OC-SPECIFIC OR -RELATED EXPRESSED GENES (cDNA CLONES)

34A (SEQ ID NO: 1)						
1	GCAAATATCT	AAGTTTATTG	CTTGGATTTC	TAGTGAGAGC	TGTTGAATTT	GGTGATGTCA
61	AATGTTTCTA	GGGTTTTTTT	AGTTTGTTTT	TATTGAAAAA	TTTAATTATT	TATGCTATAG
121	GTGATATTCT	CTTTGAATAA	ACCTATAATA	GAAAATAGCA	GCAGACAACA	
4B (SEQ ID NO: 2)						
1	GTGTCAACCT	GCATATCCTA	AAAATGTCAA	AATGCTGCAT	CTGGTTAATG	TCGGGGTAGG

TABLE I-continued

PARTIAL SEQUENCES OF 32 NOVEL OC-SPECIFIC OR -RELATED EXPRESSED GENES (cDNA CLONES)

61	GGG					
12B (SEQ ID NO: 3)						
1	CTTCCCTCTC	TTGCTTCCCT	TTCCCAAGCA	GAGGTGCTCA	CTCCATGGCC	ACCGCCACCA
61	CAGGCCCACA	GGGAGTACTG	CCAGACTACT	GCTGATGTTC	TCTTAAGGCC	CAGGGAGTCT
121	CAACCAGCTG	GTGGTGAATG	CTGCCTGGCA	CGGGACCCCC	CCC	
28B (SEQ ID NO: 4)						
1	TTTTATTTGT	AAATATATGT	ATTACATCCC	TAGAAAAAGA	ATCCCAGGAT	TTTCCCTCCT
61	GTGTGTTTTC	GTCTTGCTTC	TTCATGGTCC	ATGATGCCAG	CTGAGGTTGT	CAGTACAATG
121	AAACCAAACT	GGCGGGATGG	AAGCAGATTA	TTCTGCCATT	TTTCCAGGTC	TTT
37B (SEQ ID NO: 5)						
1	GGCTGGACAT	GGGTGCCCTC	CACGTCCCTC	ATATCCCCAG	GCACACTCTG	GCCTCAGGTT
61	TTGCCCTGGC	CATGTCATCT	ACCTGGAGTG	GGCCCTCCCCC	TTCTTCAGCC	TTGAATCAAA
121	AGCCACTTTG	TTAGGCGAGG	ATTTCCCAGA	CCACTCATCA	CATTAAAAAA	TATTTTGAAA
181	ACAAAAAAAA	AAAAAAA				
55B (SEQ ID NO: 6)						
1	TTGACAAAGC	TGTTTATTTC	CACCAATAAA	TAGTATATGG	TGATTGGGGT	TTCTATTTAT
61	AAGAGTAGTG	GCTATTATAT	GGGGTATCAT	GTTGATGCTC	ATAAATAGTT	CATATCTACT
121	TAATTTGCCT	TC				
60B (SEQ ID NO: 7)						
1	GAAGAGAGTT	GTATGTACAA	CCCCAACAGG	CAAGGCAGCT	AAATGCAGAG	GGTACAGAGA
61	GATCCCGAGG	GAATT				
86B (SEQ ID NO: 8)						
1	GGATGGAAAC	ATGTAGAAGT	CCAGAGAAAA	ACAATTTTAA	AAAAAGGTGG	AAAAGTTACG
61	GCAAACCTGA	GATTTCAGCA	TAAAATCTTT	AGTTAGAAGT	GAGAGAAAGA	AGAGGGAGGC
121	TGGTTGCTGT	TGCACGTATC	AATAGGTTAT	C		
87B (SEQ ID NO: 9)						
1	TTCTTGATCT	TTAGAACACT	ATGAATAGGG	AAAAAAGAAA	AAACTGTTCA	AAATAAAATG
61	TAGGAGCCGT	GCTTTTGGAA	TGCTTGAGTG	AGGAGCTCAA	CAAGTCCTCT	CCCAAGAAAG
181	CAATGATAAA	ACTTGACAAA	A			
98B (SEQ ID NO: 10)						
1	ACCCATTTCT	AACAATTTTT	ACTGTAAAAT	TTTTGGTCAA	AGTTCTAAGC	TTAATCACAT
61	CTCAAAGAAT	AGAGGCAATA	TATAGCCCAT	CTTACTAGAC	ATACAGTATT	AAACTGGACT
121	GAATATGAGG	ACAAGCTCTA	GTGGTCATTA	AACCCCTCAG	AA	
110B (SEQ ID NO: 11)						
1	ACATATATTA	ACAGCATTCA	TTTGGCCAAA	ATCTACACGT	TTGTAGAATC	CTACTGTATA
61	TAAAGTGGGA	ATGTATCAAG	TATAGACTAT	GAAAGTGCAA	ATAACAAGTC	AAGGTTAGAT
121	TAACTTTTTT	TTTTTACATT	ATAAAATTAA	CTTGTTT		
118B (SEQ ID NO: 12)						
1	CCAAATTTCT	CTGGAATCCA	TCCTCCCTCC	CATCACCATA	GCCTCGAGAC	GTCATTTCTG
61	TTTGACTACT	CCAGC				
133B (SEQ ID NO: 13)						
1	AACTAACCTC	CTCGGACCCC	TGCCTCACTC	ATTTACACCA	ACCACCCAAC	TATCTATAAA
61	CCTGAGCCAT	GGCCATCCCT	TATGAGCGGC	GCAGTGATTA	TAGGCTTTCG	CTCTAAGATA
121	AAAT					
140B (SEQ ID NO: 14)						
1	ATTATTATTC	TTTTTTTATG	TTAGCTTAGC	CATGCAAAAT	TTACTGGTGA	AGCAGTTAAT
61	AAAACACACA	TCCCATTGAA	GGGTTTTGTA	CATTTCAGTC	CTTACAAATA	ACAAAGCAAT
121	GATAAACCCG	GCACGTCCTG	ATAGGAAATT	C		
144B (SEQ ID NO: 15)						
1	CGTGACACAA	ACATGCATTC	GTTTTATTCA	TAAAACAGCC	TGGTTTCCTA	AAACAATACA
61	AACAGCATGT	TCATCAGCAG	GAAGCTGGCC	GTGGGCAGGG	GGGCC	
198B[a] (SEQ ID NO: 16)						
1	ATAGGTTAGA	TTCTCATTCA	CGGGACTAGT	TAGCTTTAAG	CACCCTAGAG	GACTAGGGTA
61	ATCTGACTTC	TCACTTCCTA	AGTTCCCTCT	TATATCCTCA	AGGTAGAAAT	GTCTATGTTT
121	TCTACTCCAA	TTCATAAATC	TATTCATAAG	TCTTTGGTAC	AAGTTACATG	ATAAAAAGAA
181	ATGTGATTTG	TCTTCCCTTC	TTTGCACTTT	TRAAATAAAG	TATTTATCTC	CTGTCTACAG
241	TTTAAT					
212B (SEQ ID NO: 17)						
1	GTCCAGTATA	AAGGAAAGCG	TTAAGTCGGT	AAGCTAGAGG	ATTGTAAATA	TCTTTTATGT
61	CCTCTAGATA	AAACACCCGA	TTAACAGATG	TTAACCTTTT	ATGTTTTGAT	TTGCTTTAAA
121	AATGGCCTTC	TACACATTAG	CTCCAGCTAA	AAAGACACAT	TGAGAGCTTA	GAGGATAGTC
181	TCTGGAGC					
223B[b] (SEQ ID NO: 18)						
1	GCACTTGGAA	GGGAGTTGGT	GTGCTATTTT	TGAAGCAGAT	GTGGTGATAC	TGAGATTGTC
61	TGTTCAGTTT	CCCCATTTGT	TTGTGCTTCA	AATGATCCTT	CCTACTTTGC	TTCTCTCCAC
121	CCATGACCTT	TTTCACTGTG	GCCATCAAGG	ACTTTCCTGA	CAGCTTGTGT	ACTCTTAGGC
181	TAAGAGATGT	GACTACAGCC	TGCCCCTGAC	TG		
241B (SEQ ID NO: 19)						
1	TGTTAGTTTT	TAGGAAGGCC	TGTCTTCTGG	GAGTGAGGTT	TATTAGTCCA	CTTCTTGGAG
61	CTAGACGTCC	TATAGTTAGT	CACTGGGGAT	GGTGAAAGAG	GGAGAAGAGG	AAGGGCGAAG
121	GGAAGGGCTC	TTTGCTAGTA	TCTCCATTTC	TAGAAGATGG	TTTAGATGAT	AACCACAGGT
181	CTATATGAGC	ATAGTAAGGC	TGT			
32C[c] (SEQ ID NO: 20)						
1	CCTATTTCTG	ATCCTGACTT	TGGACAAGGC	CCTTCAGCCA	GAAGACTGAC	AAAGTCATCC
121	TCCGTCTACC	AGAGCGTGCA	CTTGTGATCC	TAAAATAAGC	TTCATCTCCG	GCTGTGCCTT
161	GGGTGGAAGG	GGCAGGATTC	TGCAGCTGCT	TTTGCATTTC	TCTTCCTAAA	TTTCATT

TABLE I-continued

PARTIAL SEQUENCES OF 32 NOVEL OC-SPECIFIC OR -RELATED EXPRESSED GENES (cDNA CLONES)

34C (SEQ ID NO: 21)						
1	CGGAGCGTAG	GTGTGTTTAT	TCCTGTACAA	ATCATTACAA	AACCAAGTCT	GGGGCAGTCA
61	CCGCCCCCAC	CCATCACCCC	AGTGCAATGG	CTAGCTGCTG	GCCTTT	
47C (SEQ ID NO: 22)						
1	TTAGTTCAGT	CAAAGCAGGC	AACCCCCTTT	GGCACTGCTG	CCACTGGGGT	CATGGCGGTT
61	GTGGCAGCTG	GGGAGGTTTC	CCCAACACCC	TCCTCTGCTT	CCCTGTGTGT	CGGGGTCTCA
121	GGAGCTGACC	CAGAGTGGA				
65C (SEQ ID NO: 23)						
1	GCTGAATGTT	TAAGAGAGAT	TTTGGTCTTA	AAGGCTTCAT	CATGAAAGTG	TACATGCATA
61	TGCAAGTGTG	AATTACGTGG	TATGGATGGT	TGCTTGTTTA	TTAACTAAAG	ATGTACAGCA
121	AACTGCCCGT	TTAGAGTCCT	CTTAATATTG	ATGTCCTAAC	ACTGGGTCTG	CTTATGC
79C (SEQ ID NO: 24)						
1	GGCAGTGGGA	TATGGAATCC	AGAAGGGAAA	CAAGCACTGG	ATAATTAAAA	ACAGCTGGGG
61	AGAAAACTGG	GGAAACAAAG	GATATATCCT	CATGGCTCGA	AATAAGAACA	ACGCCTGTGG
121	CATTGCCAAC	CTGGCCAGCT	TCCCCAAGAT	GTGACTCCAG	CCAGAAA	
84C (SEQ ID NO: 25)						
1	GCCAGGGCGG	ACCGTCTTTA	TTCCTCTCCT	GCCTCAGAGG	TCAGGAAGGA	GGTCTGGCAG
61	GACCTGCAGT	GGGCCCTAGT	CATCTGTGGC	AGCGAAGGTG	AAGGGACTCA	CCTTGTCGCC
121	CGTGCCTGAG	TAGAACTTGT	TCTGGAATTC	C		
86C (SEQ ID NO: 26)						
1	AACTCTTTCA	CACTCTGGTA	TTTTTAGTTT	AACAATATAT	GTGTTGTGTC	TTGGAAATTA
61	GTTCATATCA	ATTCATATTG	AGCTGTCTCA	TTCTTTTTTT	AATGGTCATA	TACAGTAGTA
121	TTCAATTATA	AGAATATATC	CTAATACTTT	TTAAAA		
87C (SEQ ID NO: 27)						
1	GGATAAGAAA	GAAGGCCTGA	GGCCTAGGGG	CCGRGGCTGG	CCTGCGTCTC	AGTCCTGGGA
61	CGCAGCAGCC	CGCACAGGTT	GAGAGGGGCA	CTTCCTCTTG	CTTAGGTTGG	TGAGGATCTG
121	GTCCTGGTTG	GCCGGTGGAG	AGCCACAAAA			
88C (SEQ ID NO: 28)						
1	CTGACCTTCG	AGAGTTTGAC	CTGGAGCCGG	ATACCTACTG	CCGCTATGAC	TCGGTCAGCG
61	TGTTCAACGG	AGCCGTGAGC	GACGACTCCG	GTGGGGAAGT	TCTGCGGCGA	T
89C (SEQ ID NO: 29)						
1	ATCCCTGGCT	GTGGATAGTG	CTTTTGTGTA	GCAAATGCTC	CCTCCTTAAG	GTTATAGGGC
61	TCCCTGAGTT	TGGGAGTGTG	GAAGTACTAC	TTAACTGTCT	GTCCTGCTTG	GCTGTGGTTA
121	TCGTTTTCTG	GTGATGTTGT	GCTAACAATA	AGAATAC		
101C (SEQ ID NO: 30)						
1	GGCTGGGCAT	CCCTCTCCTC	CTCCATCCCC	ATACATCACC	AGGTCTAATG	TTTACAAACG
61	GTGCCAGCCC	GGCTCTGAAG	CCAAGGGCCG	TCCGTGCCAC	GGTGGCTGTG	AGTATTCCTC
121	CGTTAGCTTT	CCCATAAGGT	TGGAGTATCT	GC		
112C (SEQ ID NO: 31)						
1	CCAACTCCTA	CCGCGATACA	GACCCACAGA	GTGCCATCCC	TGAGAGACCA	GACCGCTCCC
161	CAATACTCTC	CTAAAATAAA	CATGAAGCAC			
114C (SEQ ID NO: 32)						
1	CATGGATGAA	TGTCTCATGG	TGGGAAGGAA	CATGGTACAT	TTC	

[a]Repeated 3 times
[b]Repeated 2 times

Sequence analysis of the OC^+ stromal $cell^-$ cloned DNA sequences revealed, in addition to the novel sequences, a number of previously-described genes. The known genes identified (including type 5 acid phosphatase, gelatinase B, cystatin C (13 clones), Alu repeat sequences (11 clones), creatnine kinase (6 clones) and others) are summarized in Table II. In situ hybridization (described below) directly demonstrated that gelatinase B mRNA is expressed in multinucleated osteoclasts and not in stromal cells. Although gelatinase B is a well-characterized protease, its expression at high levels in osteoclasts has not been previously described. The expression in osteoclasts of cystatin C, a cysteine protease inhibitor, is also unexpected. This finding has not yet been confirmed by in situ hybridization. Taken together, these results demonstrate that most of these identified genes are osteoclast-expressed, thereby confirming the effectiveness of the differential screening strategy for identifying DNA encoding osteoclast-specific or -related gene products. Therefore, novel genes identified by this method have a high probability of being OC-specific or related.

In addition, a minority of the genes identified by this screen are probably not expressed by OCs (Table II). For example, type III collagen (6 clones), collagen type I (1 clone), dermatansulfate (1 clone), and type VI collagen (1 clone) are more likely to originate from the stromal cells or from osteoblastic cells which are present in the tumor. These cDNA sequences survive the differential screening process either because the cells which produce them in the tumor in vivo die out during the stromal cell propagation phase, or because they stop producing their product in vitro. These clones do not constitute more than 5–10% of the all sequences selected by differential hybridization.

TABLE II

SEQUENCE ANALYSIS OF CLONES ENCODING KNOWN SEQUENCES FROM AN OSTEOCLASTOMA cDNA LIBRARY

Clones with Sequence Homology to Collagenase Type IV	25 total
Clones with Sequence Homology to Type 5 Tartrate Resistant Acid Phosphatase	14 total
Clones with Sequence Homology to Cystatin C:	13 total
Clones with Sequence Homology to Alu-repeat Sequences	11 total
Clones with Sequence Homology to Creatnine Kinase	6 total
Clones with Sequence Homology to	6 total

TABLE II-continued

SEQUENCE ANALYSIS OF CLONES ENCODING KNOWN SEQUENCES FROM AN OSTEOCLASTOMA cDNA LIBRARY

Type III Collagen	
Clones with Sequence Homology to MHC Class I γ Invariant Chain	5 total
Clones with Sequence Homology to MHC Class II β Chain	3 total
One or Two Clone(s) with Sequence Homology to Each of the Following:	10 total
αI collagen type I	
γ interferon inducible protein	
osteopontin	
Human chondroitin/dermatansulfate	
α globin	
β glucosidase/sphingolipid activator	
Human CAPL protein (Ca binding)	
Human EST 01024	
Type VI collagen	
Human EST 00553	

Example 5—In situ Hybridiation of OC-Expressed Genes

In situ hybridization was performed using probes derived from novel cloned sequences in order to determine whether the novel putative OC-specific or -related genes are differentially expressed in osteoclasts (and not expressed in the stromal cells) of human giant cell tumors. Initially, in situ hybridization was performed using antisense (positive) and sense (negative control) cRNA probes against human type IV collagenase/gelatinase B labelled with ^{35}S-UTP.

A thin section of human giant cell tumor reacted with the antisense probe resulted in intense labelling of all OCs, as indicated by the deposition of silver grains over these cells, but failed to label the stromal cell elements. In contrast, only minimal background labelling was observed with the sense (negative control) probe. This result confirmed that gelatinase B is expressed in human OCs.

In situ hybridization was then carried out using cRNA probes derived from 11/32 novel genes, labelled with digoxigenin UTP according to known methods.

The results of this analysis are summarized in Table III. Clones 28B, 118B, 140B, 198B, and 212B all gave positive reactions with OCs in frozen sections of a giant cell tumor, as did the positive control gelatinase B. These novel clones therefore are expressed in OCs and fulfill all criteria for OC-relatedness. 198B is repeated three times, indicating relatively high expression. Clones 4B, 37B, 88C and 98B produced positive reactions with the tumor tissue; however the signal was not well-localized to OCs. These clones are therefore not likely to be useful and are eliminated from further consideration. Clones 86B and 87B failed to give a positive reaction with any cell type, possibly indicating very low level expression. This group of clones could still be useful but may be difficult to study further. The results of this analysis show that 5/11 novel genes are expressed in OCs, indicating that ~50% of novel sequences likely to be OC-related.

To generate probes for the in situ hybridizations, cDNA derived from novel cloned osteoclast-specific or -related cDNA was subcloned into a BlueScript II SK(−) vector. The orientation of cloned inserts was determined by restriction analysis of subclones. The T7 and T3 promoters in the BlueScriptII vector was used to generate ^{35}S-labelled (^{35}S-UTP 850 Ci/mmol, Amersham, Arlington Heights, Ill.), or UTP digoxygenin labelled cRNA probes.

TABLE III

In Situ HYBRIDIZATION USING PROBES DERIVED FROM NOVEL SEQUENCES

Clone	Reactivity with: Osteoclasts	Stromal Cells
4B	+	+
28B*	+	−
37B	+	+
86B	−	−
87B	−	−
88C	+	+
98B	+	+
118B*	+	−
140B*	+	−
198B*	+	−
212B*	+	−
Gelatinase B*	+	−

*OC-expressed, as indicated by reactivity with antisense probe and lack of reactivity with sense probe on OCs only.

In situ hybridization was carried out on 7 micron cryostat sections of a human osteoclastoma as described previously (Chang, L.-C. et al. *Cancer Res.* 49:6700 (1989)). Briefly, tissue was fixed in 4% paraformaldehyde and embedded in OCT (Miles Inc., Kankakee, Ill.). The sections were rehydrated, postfixed in 4% paraformaldehyde, washed, and pretreated with 10 mM DTT, 10 mM iodoacetamide, 10 mM N-ethylmaleimide and 0.1 triethanolamine-HCL. Prehybridization was done with 50% deionized formamide, 10 mM Tris-HCl, pH 7.0, 1× Denhardt's, 500 mg/ml tRNA, 80 mg/ml salmon sperm DNA, 0.3M NaCl, mM EDTA, and 100 mM DTT at 45° C. for 2 hours. Fresh hybridization solution containing 10% dextran sulfate and 1.5 ng/ml ^{35}S-labelled or digoxygenin labelled RNA probe was applied after heat denaturation. Sections were coverslipped and then incubated in a moistened chamber at 45°–50° C. overnight. Hybridized sections were washed four times with 50% formamide, 2× SSC, containing 10 mM DTT and 0.5% Triton X-100 at 45° C. Sections were treated with RNase A and RNase T1 to digest single-stranded RNA, washed four times in 2× SSC/10 mM DTT.

In order to detect ^{35}S-labelling by autoradiography, slides were dehydrated, dried, and coated with Kodak NTB-2 emulsion. The duplicate slides were split, and each set was placed in a black box with desiccant, sealed, and incubated at 4° C. for 2 days. The slides were developed (4 minutes) and fixed (5 minutes) using Kodak developer D19 and Kodak fixer. Hematoxylin and eosin were used as counterstains.

In order to detect digoxygenin-labelled probes, a Nucleic Acid Detection Kit (Boehringer-Mannheim, Cat. #1175041) was used. Slides were washed in Buffer 1 consisting of 100 mM Tris/150 mM NaCl, pH7.5, for 1 minute. 100 µl Buffer 2 was added (made by adding 2 mg/ml blocking reagent as provided by the manufacturer) in Buffer 1 to each slide. The slides were placed on a shaker and gently swirled at 20° C.

Antibody solutions were diluted 1:100 with Buffer 2 (as provided by the manufacturer). 100 µl of diluted antibody solution was applied to the slides and the slides were then incubated in a chamber for 1 hour at room temperature. The slides were monitored to avoid drying. After incubation with antibody solution, slides were washed in Buffer 1 for 10 minutes, then washed in Buffer 3 containing 2 mM levamisole for 2 minutes.

After washing, 100 µl color solution was added to the slides. Color solution consisted of nitroblue/tetrazolium salt

(NBT) (1:225 dilution) 4.5 μl, 5-bromo-4-chloro-3-indolyl phosphate (1:285 dilution) 3.5 μl, levamisole 0.2 mg in Buffer 3 (as provided by the manufacturer) in a total volume of 1 ml. Color solution was prepared immediately before use.

After adding the color solution, the slides were placed in a dark, humidified chamber at 20° C. for 2–5 hours and monitored for color development. The color reaction was stopped by rinsing slides in TE Buffer.

The slides were stained for 60 seconds in 0.25% methyl green, washed with tap water, then mounted with water-based Permount (Fisher).

Example 6—Immunohistochemistry

Immunohistochemical staining was performed on frozen and paraffin embedded tissues as well as on cytospin preparations (see Table IV). The following antibodies were used: polyclonal rabbit anti-human gelatinase antibodies; Ab110 for gelatinase B; monoclonal mouse anti-human CD68 antibody (clone KP1) (DAKO, Denmark); Mol (anti-CD11b) and Mo2 (anti-CD14) derived from ATCC cell lines HB CRL 8026 and TIB 228/HB44. The anti-human gelatinase B antibody Ab110 was raised against a synthetic peptide with the amino acid sequence EALMYPMYRFTEGPPLHK (SEQ ID NO: 34), which is specific for human gelatinase B (Corcoran, M. L. et al. *J. Biol. Chem*, 267:515 (1992)).

Detection of the immunohistochemical staining was achieved by using a goat anti-rabbit glucose oxidase kit (Vector Laboratories, Burlingame Calif.) according to the manufacturer's directions. Briefly, the sections were rehydrated and pretested with either acetone or 0.1% trypsin. Normal goat serum was used to block nonspecific binding. Incubation with the primary antibody for 2 hours or overnight (Abl10:1/500 dilution) was followed by either a glucose oxidase labeled secondary anti-rabbit serum, or, in the case of the mouse monoclonal antibodies, were reacted with purified rabbit anti-mouse Ig before incubation with the secondary antibody.

Paraffin embedded and frozen sections from osteoclastomas (GCT) were reacted with a rabbit antiserum against gelatinase B (antibody 110) (Corcoran, M. L. et al. *J. Biol. chem.* 267:515 (1992)), followed by color development with glucose oxidase linked reagents. The osteoclasts of a giant cell tumor were uniformly strongly positive for gelatinase B, whereas the stromal cells were unreactive. Control sections reacted with rabbit preimmune serum were negative. Identical findings were obtained for all 8 long bone giant cell tumors tested (Table IV). The osteoclasts present in three out of four central giant cell granulomas (GCG) of the mandible were also positive for gelatinase B expression. These neoplasms are similar but not identical to the long bone giant cell tumors, apart from their location in the jaws (Shafer, W. G. et al., Textbook of Oral Pathology, W. B. Saunders Company, Philadelphia, pp. 144–149 (1983)). In contrast, the multinucleated cells from a peripheral giant cell tumor, which is a generally non-resorptive tumor of oral soft tissue, were unreactive with antibody (Shafer, W. G. et. al., Textbook of Oral Pathology, W. B. Saunders Company, Philadelphia, pp. 144–149 (1983)).

Antibody 110 was also utilized to assess the presence of gelatinase B in normal bone (n=3) and in Paget's disease, in which there is elevated bone remodeling and increased osteoclastic activity. Strong staining for gelatinase B was observed in osteoclasts both in normal bone (mandible of a 2 year old), and in Paget's disease. Staining was again absent in controls incubated with preimmune serum. Osteoblasts did not stain in any of the tissue sections, indicating that gelatinase B expression is limited to osteoclasts in bone. Finally, peripheral blood monocytes were also reactive with antibody 110 (Table IV).

TABLE IV

DISTRIBUTION OF GELATINASE B IN VARIOUS TISSUES

Samples	Antibodies tested Ab 110 gelatinase B
GCT frozen (n = 2)	
giant cells	+
stromal cells	–
GCT paraffin (n = 6)	
giant cells	+
stromal cells	–
central GCG (n = 4)	
giant cells	+(¾)
stromal cells	–
peripheral GCT (n = 4)	
giant cells	–
stromal cells	–
Paget's disease (n = 1)	
osteoclasts	+
osteoblasts	–
normal bone (n = 3)	
osteoclasts	+
osteoblasts	–
monocytes (cytospin)	+

Distribution of gelatinase B in multinucleated giant cells, osteoclasts, osteoblasts and stromal cells in various tissues. In general, paraffin embedded tissues were used for these experiments; exceptions are indicated.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments described herein. Such equivalents are intended to be encompassed by the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i i i) NUMBER OF SEQUENCES: 34

-continued

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAAATATCT AAGTTTATTG CTTGGATTTC TAGTGAGAGC TGTTGAATTT GGTGATGTCA 60

AATGTTTCTA GGGTTTTTTT AGTTTGTTTT TATTGAAAAA TTTAATTATT TATGCTATAG 120

GTGATATTCT CTTTGAATAA ACCTATAATA GAAAATAGCA GCAGACAACA 170

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGTCAACCT GCATATCCTA AAAATGTCAA AATGCTGCAT CTGGTTAATG TCGGGGTAGG 60

GGG 63

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTCCCTCTC TTGCTTCCCT TTCCCAAGCA GAGGTGCTCA CTCCATGGCC ACCGCCACCA 60

CAGGCCCACA GGGAGTACTG CCAGACTACT GCTGATGTTC TCTTAAGGCC CAGGGAGTCT 120

CAACCAGCTG GTGGTGAATG CTGCCTGGCA CGGGACCCCC CCC 163

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTATTTGT AAATATATGT ATTACATCCC TAGAAAAAGA ATCCCAGGAT TTTCCCTCCT 60

GTGTGTTTTC GTCTTGCTTC TTCATGGTCC ATGATGCCAG CTGAGGTTGT CAGTACAATG 120

AAACCAAACT GGCGGGATGG AAGCAGATTA TTCTGCCATT TTTCCAGGTC TTT 173

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

-continued

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCTGGACAT GGGTGCCCTC CACGTCCCTC ATATCCCCAG GCACACTCTG GCCTCAGGTT 60

TTGCCCTGGC CATGTCATCT ACCTGGAGTG GGCCCTCCCC TTCTTCAGCC TTGAATCAAA 120

AGCCACTTTG TTAGGCGAGG ATTTCCCAGA CCACTCATCA CATTAAAAAA TATTTTGAAA 180

ACAAAAAAAA AAAAAAA 197

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGACAAAGC TGTTTATTTC CACCAATAAA TAGTATATGG TGATTGGGGT TTCTATTTAT 60

AAGAGTAGTG GCTATTATAT GGGGTATCAT GTTGATGCTC ATAAATAGTT CATATCTACT 120

TAATTTGCCT TC 132

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGAGAGTT GTATGTACAA CCCCAACAGG CAAGGCAGCT AAATGCAGAG GGTACAGAGA 60

GATCCCGAGG GAATT 75

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGATGGAAAC ATGTAGAAGT CCAGAGAAAA ACAATTTTAA AAAAAGGTGG AAAAGTTACG 60

GCAAACCTGA GATTTCAGCA TAAAATCTTT AGTTAGAAGT GAGAGAAAGA AGAGGGAGGC 120

TGGTTGCTGT TGCACGTATC AATAGGTTAT C 151

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

-continued

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCTTGATCT TTAGAACACT ATGAATAGGG AAAAAAGAAA AAACTGTTCA AAATAAAATG 60

TAGGAGCCGT GCTTTTGGAA TGCTTGAGTG AGGAGCTCAA CAAGTCCTCT CCCAAGAAAG 120

CAATGATAAA ACTTGACAAA A 141

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACCCATTTCT AACAATTTTT ACTGTAAAAT TTTTGGTCAA AGTTCTAAGC TTAATCACAT 60

CTCAAAGAAT AGAGGCAATA TATAGCCCAT CTTACTAGAC ATACAGTATT AAACTGGACT 120

GAATATGAGG ACAAGCTCTA GTGGTCATTA AACCCCTCAG AA 162

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACATATATTA ACAGCATTCA TTTGGCCAAA ATCTACACGT TTGTAGAATC CTACTGTATA 60

TAAAGTGGGA ATGTATCAAG TATAGACTAT GAAAGTGCAA ATAACAAGTC AAGGTTAGAT 120

TAACTTTTTT TTTTTACATT ATAAAATTAA CTTGTTT 157

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCAAATTTCT CTGGAATCCA TCCTCCCTCC CATCACCATA GCCTCGAGAC GTCATTTCTG 60

TTTGACTACT CCAGC 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACTAACCTC CTCGGACCCC TGCCTCACTC ATTTACACCA ACCACCCAAC TATCTATAAA 60

CCTGAGCCAT GGCCATCCCT TATGAGCGGC GCAGTGATTA TAGGCTTTCG CTCTAAGATA 120

-continued

AAAT 124

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATTATTATTC TTTTTTTATG TTAGCTTAGC CATGCAAAAT TTACTGGTGA AGCAGTTAAT 60

AAAACACACA TCCCATTGAA GGGTTTTGTA CATTTCAGTC CTTACAAATA ACAAAGCAAT 120

GATAAACCCG GCACGTCCTG ATAGGAAATT C 151

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGTGACACAA ACATGCATTC GTTTTATTCA TAAAACAGCC TGGTTTCCTA AAACAATACA 60

AACAGCATGT TCATCAGCAG GAAGCTGGCC GTGGGCAGGG GGGCC 105

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATAGGTTAGA TTCTCATTCA CGGGACTAGT TAGCTTTAAG CACCCTAGAG GACTAGGGTA 60

ATCTGACTTC TCACTTCCTA AGTTCCCTCT TATATCCTCA AGGTAGAAAT GTCTATGTTT 120

TCTACTCCAA TTCATAAATC TATTCATAAG TCTTTGGTAC AAGTTACATG ATAAAAAGAA 180

ATGTGATTTG TCTTCCCTTC TTTGCACTTT TGAAATAAAG TATTTATCTC CTGTCTACAG 240

TTTAAT 246

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCCAGTATA AAGGAAAGCG TTAAGTCGGT AAGCTAGAGG ATTGTAAATA TCTTTTATGT 60

CCTCTAGATA AAACACCCGA TTAACAGATG TTAACCTTTT ATGTTTTGAT TTGCTTTAAA 120

AATGGCCTTC TACACATTAG CTCCAGCTAA AAAGACACAT TGAGAGCTTA GAGGATAGTC 180

-continued

TCTGGAGC 188

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCACTTGGAA GGGAGTTGGT GTGCTATTTT TGAAGCAGAT GTGGTGATAC TGAGATTGTC 60

TGTTCAGTTT CCCCATTTGT TTGTGCTTCA AATGATCCTT CCTACTTTGC TTCTCTCCAC 120

CCATGACCTT TTTCACTGTG GCCATCAAGG ACTTTCCTGA CAGCTTGTGT ACTCTTAGGC 180

TAAGAGATGT GACTACAGCC TGCCCCTGAC TG 212

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTTAGTTTT TAGGAAGGCC TGTCTTCTGG GAGTGAGGTT TATTAGTCCA CTTCTTGGAG 60

CTAGACGTCC TATAGTTAGT CACTGGGGAT GGTGAAAGAG GGAGAAGAGG AAGGGCGAAG 120

GGAAGGGCTC TTTGCTAGTA TCTCCATTTC TAGAAGATGG TTTAGATGAT AACCACAGGT 180

CTATATGAGC ATAGTAAGGC TGT 203

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTATTTCTG ATCCTGACTT TGGACAAGGC CCTTCAGCCA GAAGACTGAC AAAGTCATCC 60

TCCGTCTACC AGAGCGTGCA CTTGTGATCC TAAAATAAGC TTCATCTCCG GCTGTGCCTT 120

GGGTGGAAGG GGCAGGATTC TGCAGCTGCT TTTGCATTTC TCTTCCTAAA TTTCATT 177

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGGAGCGTAG GTGTGTTTAT TCCTGTACAA ATCATTACAA AACCAAGTCT GGGGCAGTCA 60

CCGCCCCCAC CCATCACCCC AGTGCAATGG CTAGCTGCTG GCCTTT 106

-continued

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
TTAGTTCAGT CAAAGCAGGC AACCCCCTTT GGCACTGCTG CCACTGGGGT CATGGCGGTT      60
GTGGCAGCTG GGGAGGTTTC CCCAACACCC TCCTCTGCTT CCCTGTGTGT CGGGGTCTCA     120
GGAGCTGACC CAGAGTGGA                                                  139
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
GCTGAATGTT TAAGAGAGAT TTTGGTCTTA AAGGCTTCAT CATGAAAGTG TACATGCATA      60
TGCAAGTGTG AATTACGTGG TATGGATGGT TGCTTGTTTA TTAACTAAAG ATGTACAGCA     120
AACTGCCCGT TTAGAGTCCT CTTAATATTG ATGTCCTAAC ACTGGGTCTG CTTATGC        177
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
GGCAGTGGGA TATGGAATCC AGAAGGGAAA CAAGCACTGG ATAATTAAAA ACAGCTGGGG      60
AGAAAACTGG GGAAACAAAG GATATATCCT CATGGCTCGA AATAAGAACA ACGCCTGTGG     120
CATTGCCAAC CTGGCCAGCT TCCCCAAGAT GTGACTCCAG CCAGAAA                   167
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
GCCAGGGCGG ACCGTCTTTA TTCCTCTCCT GCCTCAGAGG TCAGGAAGGA GGTCTGGCAG      60
GACCTGCAGT GGGCCCTAGT CATCTGTGGC AGCGAAGGTG AAGGGACTCA CCTTGTCGCC     120
CGTGCCTGAG TAGAACTTGT TCTGGAATTC C                                    151
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

-continued

(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACTCTTTCA CACTCTGGTA TTTTTAGTTT AACAATATAT GTGTTGTGTC TTGGAAATTA 60

GTTCATATCA ATTCATATTG AGCTGTCTCA TTCTTTTTTT AATGGTCATA TACAGTAGTA 120

TTCAATTATA AGAATATATC CTAATACTTT TTAAAA 156

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGATAAGAAA GAAGGCCTGA GGGCTAGGGG CCGGGGCTGG CCTGCGTCTC AGTCCTGGGA 60

CGCAGCAGCC CGCACAGGTT GAGAGGGGCA CTTCCTCTTG CTTAGGTTGG TGAGGATCTG 120

GTCCTGGTTG GCCGGTGGAG AGCCACAAAA 150

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCACTTGGAA GGGAGTTGGT GTGCTATTTT TGAAGCAGAT GTGGTGATAC TGAGATTGTC 60

TGTTCAGTTT CCCCATTTGT TTGTGCTTCA AATGATCCTT CCTACTTTGC TTCTCTCCAC 120

CCATGACCTT TTTCACTGTG GCCATCAAGG ACTTTCCTGA CAGCTTGTGT ACTCTTAGGC 180

TAAGAGATGT GACTACAGCC TGCCCCTGAC TG 212

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATCCCTGGCT GTGGATAGTG CTTTTGTGTA GCAAATGCTC CCTCCTTAAG GTTATAGGGC 60

TCCCTGAGTT TGGGAGTGTG GAAGTACTAC TTAACTGTCT GTCCTGCTTG GCTGTCGTTA 120

TCGTTTTCTG GTGATGTTGT GCTAACAATA AGAATAC 157

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid

-continued

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGCTGGGCAT CCCTCTCCTC CTCCATCCCC ATACATCACC AGGTCTAATG TTTACAAACG 60

GTGCCAGCCC GGCTCTGAAG CCAAGGGCCG TCCGTGCCAC GGTGGCTGTG AGTATTCCTC 120

CGTTAGCTTT CCCATAAGGT TGGAGTATCT GC 152

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCAACTCCTA CCGCGATACA GACCCACAGA GTGCCATCCC TGAGAGACCA GACCGCTCCC 60

CAATACTCTC CTAAAATAAA CATGAAGCAC 90

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CATGGATGAA TGTCTCATGG TGGGAAGGAA CATGGTACAT TTC 43

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCCTG GTCCTGGTGC TCCTGGTGCT 60

GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA 120

CCTGAGAACC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180

CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT 240

CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300

GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGGCAGATTC CAAACCTTTG AGGGCGACCT 360

CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG 420

GGCGGTGATT GACGACGCCT TTGCCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCCGCT 480

CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTCGCGGA 540

GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC 600

TGGCCCCGGC ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA 660

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```
GGGCGTCGTG GTTCCAACTC GGTTTGGAAA CGCAGATGGC GCGGCCTGCC ACTTCCCCTT    720
CATCTTCGAG GGCCGCTCCT ACTCTGCCTG CACCACCGAC GGTCGCTCCG ACGGGTTGCC    780
CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA    840
GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCATCTT    900
CCAAGGCCAA TCCTACTCCG CCTGCACCAC GGACGGTCGC TCCGACGGCT ACCGCTGGTG    960
CGCCACCACC GCCAACTACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCCGAGCTGA   1020
CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCCT TCACTTTCCT   1080
GGGTAAGGAG TACTCGACCT GTACCAGCGA GGGCCGCGGA GATGGGCGCC TCTGGTGCGC   1140
TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG   1200
TTTGTTCCTC GTGGCGGCGC ATGAGTTCGG CCACGCGCTG GGCTTAGATC ATTCCTCAGT   1260
GCCGGAGGCG CTCATGTACC CTATGTACCG CTTCACTGAG GGGCCCCCCT TGCATAAGGA   1320
CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCCTCC   1380
AACCACCACC ACACCGCAGC CCACGGCTCC CCCGACGGTC TGCCCCACCG GACCCCCCAC   1440
TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC   1500
AGGTCCCCCC ACTGCTGGCC CTTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA   1560
TGCCTGCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGGAACCAGC TGTATTTGTT   1620
CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCCGGCCGC AGGGCCCCTT   1680
CCTTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC   1740
GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC   1800
GGTGCTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC   1860
CGGGGCCCTC CGGAGTGGCA GGGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG   1920
GTTCGACGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT   1980
CCCCGGGGTG CCTTTGGACA CGCACGACGT CTTCCAGTAC CGAGAGAAAG CCTATTTCTG   2040
CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACCAGG TGGACCAAGT   2100
GGGCTACGTG ACCTATGACA TCCTGCAGTG CCCTGAGGAC TAGGGCTCCC GTCCTGCTTT   2160
GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA   2220
CAAACTGGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC   2280
TCACCTTTGT TTTTTGTTGG AGTGTTTCTA ATAAACTTGG ATTCTCTAAC CTTT          2334
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(i i) MOLECULE TYPE: peptide

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Glu Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu
 1               5                  10                  15

His Lys
```

We claim:

1. An isolated osteoclast-specific or -related DNA sequence, or its complementary sequence, the DNA sequence comprising a nucleic acid sequence selected from the group consisting of:

a) DNA sequences set forth in the group consisting of SEQ ID NOS. 12, 14, 16 and 17, or their complementary strands; and

b) DNA sequences which hybridize under standard conditions to the DNA sequences defined in a).

2. A DNA construct capable of replicating, in a host cell, osteoclast-specific or -related DNA, said construct comprising:

a) a DNA sequence of claim 1; and

b) sequences, in addition to said DNA sequence, necessary for transforming or transfecting a host cell, and for replicating, in a host cell, said DNA sequence.

3. A DNA construct capable or replicating and expressing, in a host cell, osteoclast-specific or -related DNA, said construct comprising:

a) a DNA sequence of claim 2; and

b) sequences, in addition to said DNA sequence, necessary for transforming or transfecting a host cell, and for replicating and expressing, in a host cell, said DNA sequence.

4. A cell stably transformed or transfected with a DNA construct according to claim 3.

5. A cell stably transformed or transfected with a DNA construct according to claim 4.

* * * * *